

TITLE

Design and use of two pooled tissue normalized cDNA libraries

Design and use of two pooled tissue normalized cDNA libraries for

Email: cnapbs@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM9743 row: 1 column: 14
 High quality sequence stop: 729.
 Location/Qualifiers
 1. 825
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3917293"
 /clone_lib="NIH_MGC_72"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."

FEATURES
 source

BASE COUNT 187 a 220 c 293 g 125 t
 ORIGIN

Query Match 22.98; Score 689; DB 141; Length 825;
 Best Local Similarity 98.48; Pred. No. 5.3e-129;
 Matches 711; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

Oy 589 gagatgctcagcctctcgtcactatagcgaatgcgtgcaggaagagctgcccgc 648
 Db 1 CAGATGCTCAGCCTCTCGCTGCATATAGCAATGCTGCAGGACAGAGCTGCCGCC 60
 Oy 649 tcacgtccgcagcctcaggaagagctgtatctactgaagcagagctgcagagacc 708
 Db 61 TCACGCTCCGAGCCTCGAGGAGGCTGTATCTACTGAAGCAGAGCTGCAGGAGCC 120
 Oy 709 aacatggttctcctcgtgagctgaatgcaagagcagctccctgaggaagcagcagac 768
 Db 121 AACATGTTTCTCTCTGTGAGCTGGAATGCAAGAGCAGTCCCTGAGGACAGCCAGCGAC 180
 Oy 769 cagagtcgaggaagagctgaacccctcgaaggaagagaatgagaacctgcgctcg 828
 Db 181 CAGGAGTCGGGGATGAGAGGCTGAACCCCTGAAGAGGAGAGAGTGCCTCGC 240
 Oy 829 ctgactttcagcctcgcgaggaagacattctgagcagagcctgcagagcgagcgaggg 888
 Db 241 CTGACTTTTCAGCCTCGCGAGAGGACATCTCTGAGCAGAGCCTGCAGAGCGGGGG 300
 Oy 889 agccgacagagagctggtgagcgcacccactcgtcgcgagcgagcgagcgagcgag 948
 Db 301 AGCCGACAGGAGCTGCTGAGCGCATCCACTCGCTGCGGAGCGGGCCCTGCTCCGAG 360
 Oy 949 aggcagcagagcagctactggaagagaaggaagcagacccctcagcttcagagaagt 1008
 Db 361 AGGCACGAGAGCAGTACTTGGGAGAGAGGAGAACACACCTCTGTCAGTTCCAGAGAGT 420
 Oy 1009 aagatggcctccaaactacagggagaaggtgaatgcgtcagagcccgaggtgtcgag 1068
 Db 421 AAGATGGCTCGCAACTCTACAGGAGAGAGTGAATGCGCTCAGGCCCGAGGTGTGCGAG 480
 Oy 1069 ctgcagaagagcagagcagcagcgttactccgcagggagacagtgctcagagggagattcc 1128
 Db 481 CTGCAGAGAGGAGCAGACAGCGCTACTCCGCGAGGAGACAGTGTCTCAGAGGAGATTTC 540
 Oy 1129 cagagcctgggtgagaaggaactccctccgcagcagcaggtgttctcagctgcagagaccaggtc 1188
 Db 541 CAGACCTGGTGGAGAGAGGACTCCCTCCGCGAGGAGGTGTCTCAGCTGACGACGAGGTC 600
 Oy 1189 tgcgagc-tgcacacacagcttcgcagctgcagcagagagcctccgggtgtgctcaagca 1247
 Db 601 TCGAGCTTGCACACACAGCTTCCGACAGCTGCAGGACAGAGCCCTCCGGGTGTGCTCAAGCA 660

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	689	22.9	825	141	BE891229	601432053
2	587	18.8	794	136	BE543447	601070755
3	421	14.0	601	165	BE291786	601084552
4	379	12.6	549	144	BF079819	230513 MA
5	276	9.2	806	144	BF100075	601752245
6	254.6	8.5	625	166	BE307936	601096060
7	164.6	5.5	243	160	BB522865	BB522865
8	164	5.4	1033	107	AU090784	AU090784
9	128.6	4.3	846	165	BE287025	601097271
10	124	4.1	513	171	BF927853	IL5-NT022
11	118.2	3.9	423	172	BG008533	PM4-GN030
12	117.6	3.9	463	119	AW654913	105416 MA
13	116	3.9	482	147	BF356060	RC1-HT088
14	114.2	3.8	494	151	BF601607	266612 MA
15	113.8	3.8	786	146	BF238116	60181836
16	111.8	3.7	1141	141	BE867544	601443043
17	110.2	3.7	412	150	BF543391	UI-R-C3-t
18	110.2	3.7	450	150	BF543402	UI-R-C3-t
19	108.6	3.6	765	108	AU142752	AU142752
20	103	3.4	560	144	BF074951	222563 MA
21	102.6	3.4	984	107	AU090785	AU090785
22	99.6	3.3	829	147	BF307399	601894035
23	99	3.3	650	241	AZ337339	IM0968803
24	98	3.3	961	173	BG105273	602312855
25	96.6	3.2	463	138	BE685413	187635 MA
26	96.6	3.2	610	136	BE513331	601315526
27	95.6	3.2	769	175	BG288547	602388013
28	90.4	3.0	605	247	AZ640388	IM0502E21
29	88	2.9	650	147	BF333601	MR2-CN003
30	84.8	2.8	447	139	BE750651	202112 MA
31	84.2	2.8	762	220	CNS01XFI	AL171639 Tetraodon
32	83.8	2.8	743	152	BG341695	602463420
33	83	2.8	552	139	BE752216	204551 MA
34	82.4	2.7	658	108	AU171861	AU171861
35	80	2.7	713	242	AZ346186	AZ346186 IM0081G06
36	79.2	2.6	377	14	AA990077	ua59a06.r
37	78.2	2.6	489	103	A1877454	u10c10.r
38	77.6	2.6	536	165	BE269246	601185484
39	76.4	2.5	168	103	A1904382	CM-BF054
40	76.4	2.5	264	103	A1904385	CM-BF054
41	76	2.5	458	4	AA285991	vb88g07.r
42	75.8	2.5	496	139	BE755039	208745 MA
43	75.4	2.5	354	20	A1447835	mr29f06.x
44	75.4	2.5	870	221	CNS03KGO	AL248145 Tetraodon
45	75.2	2.5	620	122	AW962127	EST374200

ALIGNMENTS

RESULT 1
 BE891229 825 bp mRNA EST 20-OCT-2000
 LOCUS 601432053F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917293 5', mRNA sequence.
 DEFINITION
 ACCESSION BE891229
 VERSION BE891229.1 GI:10350350
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 825)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.

Qy	875	acgaggcgagggagccgcacagagctgtgtgagcgcattccactcgtcgtcg99gagcggg	934
Db	301	ACGAGGGCGGGGAGCCGACAGGAGCTGTGTGGAGCGCATCACTCCTCGCGGAGCGGG	360
Qy	935	ccgtggctgccgagcagcagcagcagtcactgtggaagagaagaacaaccctgtgc	994
Db	361	CCGTGGCTGCCGAGAGCAGCAGCAGTACTGGGAAGAAGAAACAGACCCTGTCTGC	420
Qy	995	agttccagaagagttaatggctgcgaacctctcacagggaaggtgaatgcgctgcag	1054
Db	421	AGTTCCAGAAAGATTAAGATGGCTTGCCAACCTCTACAGGAGAAGGTGAATCGCTGCAGG	480
Qy	1055	cccaggtgtcgaaactcagaagagcagagaccagcgtagctccgcgagagacagtctc	1114
Db	481	CCCAGGTGTGGAGCTGCAGAAGGAGCGAGACCAGGCGTACTCCGCCGAGGACAGTCTC	540
Qy	1115	agaggagatttccccagagcctgttg-agaagacatccctccagcagcaggtttcag	1173
Db	541	AGAGGGAGATTTCACAGAGCTGTGTGCAGAAAGACATCCCTCCGACGACAGTGTTCGAG	600
Qy	1174	ctgacgaccaggtctctgcagctgcgcacacagcttcgcagctgcagcagcctccg	1233
Db	601	CTGACGACCAGGTCTGCGAGCTGGCACACAGCTTTCGCCAGCTTGGCGCAGAGCCCTCCG	660
Qy	1234	gggtgtccaagcaggaagccagcagcagcagcagcctgtccacgggagagcagcgg	1290
Db	661	GGTGTG---TCAAGCGGAAGCCAGGACCAGGTAGCTTGTCCACGGGAGAACGACGG	715

RESULT 3

BE291786

LOCUS BE291786 601 bp mRNA EST 13-JUL-2000

DEFINITION 601084532f1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:349865 5'

VERSION BE291786 mRNA sequence.

KEYWORDS BE291786.1 GI:9173747

SOURCE EST.

ORGANISM house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS NIH-MGC http://mgc.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAMB554 row: h column: 14
High quality sequence stop: 582.

FEATURES

source location/Qualifiers

1..601

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:349865"

/clone_lib="NCI_CGAP_Mam6"

/sex="female, virgin"

/tissue_type="infiltrating ductal carcinoma"

/dev_stage="5 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Salt; Site_2: Not; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 154 a 163 c 179 g 105 t